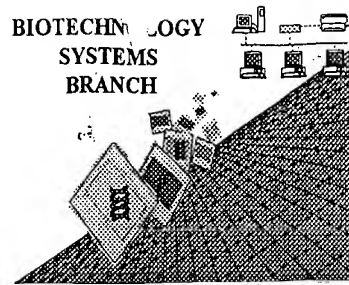


## **RAW SEQUENCE LISTING** **ERROR REPORT**

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



16 C/  
1631  
#18  
PP  
11-15-d

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

09/155,708

Source:

O/RK

Date Processed by STIC:

7/25/2001

**RECEIVED**

NOV 13 2001

TECH CENTER 1600/2900

### **THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

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## Raw Sequence Listing Error Summary

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### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER: 09/155,708

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length      The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII      The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length      Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>.<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"      A "bug" in PatentIn version 2.0 has caused the <220>.<223> section to be missing from amino acid sequences(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>.<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>.<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)      Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
    (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
    (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
    (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
    This sequence is intentionally skipped  
  
    Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)      Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
    <210> sequence id number  
    <400> sequence id number  
    000
- 9      Use of n's or Xaa's  
    (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
    Per 1.823 of Sequence Rules, use of <220>.<223> is MANDATORY if n's or Xaa's are present.  
    In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10      Invalid <213>  
    Response      Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>.<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11      Use of <220>      Sequence(s) 12 missing the <220> "Feature" and associated numeric identifiers and responses.  
    Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
    (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      Misuse of n      n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

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OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/155,708

DATE: 07/25/2001

TIME: 17:01:31

Input Set : A:\PTO\_VSK.txt

Output Set: N:\CRF3\07252001\I155708.raw

Does Not Comply  
Corrected Diskette Needed

5 <110> APPLICANT: Farrar, Jane  
 6 Humphries, Peter  
 7 Kenna, Paul  
 9 <120> TITLE OF INVENTION: Genetic Suppression and Replacement  
 11 <130> FILE REFERENCE: MUR-003  
 13 <140> CURRENT APPLICATION NUMBER: US 09/155,708  
 C--> 14 <141> CURRENT FILING DATE: 1999-04-05  
 16 <150> PRIOR APPLICATION NUMBER: PCT/GB97/00929  
 17 <151> PRIOR FILING DATE: 1997-04-02  
 19 <160> NUMBER OF SEQ ID NOS: 28  
 21 <170> SOFTWARE: PatentIn version 3.0

## ERRORED SEQUENCES

277 <210> SEQ ID NO: 8  
 278 <211> LENGTH: (649) 648  
 279 <212> TYPE: DNA  
 280 <213> ORGANISM: mammalian  
 282 <220> FEATURE:  
 W--> 283 <221> NAME/KEY: n  
 284 <222> LOCATION: (1)..(649)  
 285 <223> OTHER INFORMATION: any  
 287 <400> SEQUENCE: 8

→ group 9

E--> 288	<del>ccccctnn</del> ttttagtcnc tgccaanaaa aaaggccagc tcacaggana antananaac	(60) 59
E--> 290	ccactgctta ctggcttanc naaattaata cgactcacta tagggagacc caagcttggc	120
E--> 292	acatctgatg agtcogtgag gacgaaaaaa ttggtctaca gggccctatt ctataatgtc	180
E--> 294	acctaaatgc tanagctcgc tgatcatcct cnaactgtgcc ttctacttgc cagcctctcn	240
E--> 296	ttgtttgccc ctccccogtg ccttccttga ccctggaagg tgccactccc actgtccctt	300
E--> 298	cctaataaaa tgaggaaatt gcatgcgatt gtctgagtaa gtgtcattct attctggggg	360
E--> 300	gtgggggtggg gcaggacnnc aaaggggaag attgggaaat acaatancca agganncnctc	420
E--> 302	ccccngggta attgcggatt nggtctctntc gcttccttaa ggcngaaana aacaactnng	480
E--> 304	gcgtncggg gtttccccn ccnccctnt tagcngcgca ttantcgccg cgggtgttgt	540
E--> 306	tgttactccc cacctnaacg ctacanttgc cagcgccctaa cgccccccct tncntttctt	600
E--> 308	ccctcctttc tcncacttcc cgggttttcc ccnccaance naaatcngg	649

nos. off

Use of n and/or Xaa has been detected in the Sequence Listing.  
 Review the Sequence Listing to insure a corresponding  
 explanation is presented in the <220> to <223> fields of  
 each sequence using n or Xaa.

PVI

<210> 12

<211> 20

<212> DNA

<213> Artificial sequence

<400> 12

catcttcagc ctgggactgt

see item 11 on Eva Summary Sheet

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/155,708

DATE: 07/25/2001

TIME: 17:01:32

Input Set : A:\PTO\_VSK.txt

Output Set: N:\CRF3\07252001\I155708.raw

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
 L:29 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1  
 L:34 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
 L:36 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
 L:48 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
 L:50 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
 L:52 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
 L:62 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2  
 L:71 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
 L:73 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
 L:81 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
 L:83 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
 L:85 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
 L:87 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
 L:89 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
 L:91 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
 L:99 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3  
 L:107 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
 L:119 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
 L:121 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
 L:123 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
 L:125 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
 L:127 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
 L:129 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
 L:137 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4  
 L:142 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
 L:144 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
 L:146 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
 L:150 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
 L:152 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
 L:154 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
 L:156 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
 L:158 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
 L:160 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
 L:162 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
 L:164 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
 L:166 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
 L:168 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
 L:176 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5  
 L:181 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
 L:183 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
 L:185 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
 L:191 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
 L:193 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
 L:195 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
 L:197 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
 L:199 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
 L:201 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/155,708

DATE: 07/25/2001

TIME: 17:01:32

Input Set : A:\PTO\_VSK.txt

Output Set: N:\CRF3\07252001\I155708.raw

L:203 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:212 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6  
L:217 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:219 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:227 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:229 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:231 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:233 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:235 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:245 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7  
L:283 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8  
L:288 M:254 E: No. of Bases conflict, LENGTH:Input:60 Counted:59 SEQ:8  
M:254 Repeated in SeqNo=8  
L:308 M:252 E: No. of Seq. differs, <211>LENGTH:Input:649 Found:648 SEQ:8  
L:316 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9  
L:352 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10  
L:397 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:397 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:407 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13  
L:444 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14  
L:479 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15  
L:514 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:16  
L:553 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:17  
L:592 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:18